

S. Liu

Re-run

[Handwritten signature]



Law Sep 11/14/02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,863

DATE: 09/17/2002

TIME: 14:13:58

Input Set : N:\paola\US09697863A.RAW

Output Set: N:\CRF4\09172002\I697863.raw

ENTERED

1 <110> APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
2 <120> TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
3 <130> FILE REFERENCE: 2676-4555US
C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/697,863
5 <141> CURRENT FILING DATE: 2000-10-27
6 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03025
7 <151> PRIOR FILING DATE: 1999-04-28
8 <150> PRIOR APPLICATION NUMBER: EPO 98201392.2
9 <151> PRIOR FILING DATE: 1998-04-29
10 <160> NUMBER OF SEQ ID NOS: 6
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1920
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: misc_feature
19 <222> LOCATION: (1627)..(1627)
20 <223> OTHER INFORMATION: N stands for any nucleotide.
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (20)..(1108)
24 <223> OTHER INFORMATION:
25 <220> FEATURE:
26 <221> NAME/KEY: misc_feature
27 <222> LOCATION: (1849)..(1849)
28 <223> OTHER INFORMATION: N stands for any nucleotide.
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31 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg
32 1 5 10
33 gag gcg gcg gag gaa gag ggc gag cct gag gtg aaa aag cgg cga ctt 100
34 Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
35 15 20 25
36 ctg tgt gtg gag ttt gcc tcg gtc gca agc tgc gat gcc gca gtg gct 148
37 Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
38 30 35 40
39 cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
40 Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
41 45 50 55
42 tcc tac ttc gag cct ccg gtg gag gag agc gcc ttg gaa cgc cga cct 244
43 Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
44 60 65 70 75

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45	gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa	292
46	Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu	
47	80 85 90	
48	aca act gat tcc acc act tct aaa atc agc cca tct gaa gat act cag	340
49	Thr Thr Asp Ser Thr Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln	
50	95 100 105	
51	caa gaa aat ggc agc atg ttc tct ctc att acc tgg aat att gat gga	388
52	Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly	
53	110 115 120	
54	tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac	436
55	Leu Asp Leu Asn Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr	
56	125 130 135	
57	tta gct ttg tac agc cca gat gtg ata ttt cta cag gaa gtt att ccc	484
58	Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro	
59	140 145 150 155	
60	cca tat tat agc tac cta aag aag aga tca agt aat tat gag att att	532
61	Pro Tyr Tyr Ser Tyr Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile	
62	160 165 170	
63	aca ggt cat gaa gaa gga tat ttc aca gct ata atg ttg aag aaa tca	580
64	Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser	
65	175 180 185	
66	aga gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa	628
67	Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys	
68	190 195 200	
69	atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag	676
70	Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu	
71	205 210 215	
72	ctt tgc ctt atg aca tcc cat ttg gag agc acc aga ggg cat gct gcg	724
73	Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala	
74	220 225 230 235	
75	gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa gag gct	772
76	Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala	
77	240 245 250	
78	cca gag tca gct aca gtt ata ttt gca gga gat aca aat cta agg gat	820
79	Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp	
80	255 260 265	
81	cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc	868
82	Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val	
83	270 275 280	
84	tggt gag ttt ttg ggc aaa cct aaa cat tgc cag tat aca tgg gat aca	916
85	Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr	
86	285 290 295	
87	caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt	964
88	Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe	
89	300 305 310 315	
90	gat cga ata ttt ttc aga gca gca gca gaa gag gga cac att att ccc	1012
91	Asp Arg Ile Phe Phe Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro	
92	320 325 330	
93	cga agt ttg gac ctt ctt gga tta gaa aaa ctg gac tgt ggt aga ttt	1060

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94      Arg Ser Leu Asp Leu Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe
95              335                      340                      345
96      cct agt gat cac tgg ggt ctt ctg tgc aac tta gat ata ata ttg taa      1108
97      Pro Ser Asp His Trp Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
98              350                      355                      360
99      aatgcttttc aagtgtgggt ttgacctga ttgttgcaaa tacaatttcc accttctgga      1168
100     aaggtagggt tgctgtggag gaaataatgt actagatcat tgtcacagaa aaaccaacta      1228
101     tgatttatgg ttgtgttttc agaattcaac attaaagatt aatgtttatt taaacgaaca      1288
102     cattcctgca ttcaggatgt gaggccattt aataaaaagg gcacaaagcc tgtcagagtt      1348
103     ttcaacgggtg cttacagctg ccagctggat tccaaacagg taccctattg tctctgagct      1408
104     aatgtttata tttttccatt caggcaccga aatagttaat attttaaata agtcttcaaa      1468
105     agaaaacata agagattatt gagttcttgg gactggatcc tttatttcat aagttcagat      1528
106     catcttaaag gaaaatgccg tgattatctg cagttaaagta gatgacagct attctacatc      1588
W--> 107     agacttgatt ttgtcagct aattacataa ttggttaagnt ataattgaaa ccttatggct      1648
108     taaaattcct taactccttt ttgattcatg ttgtagtca tgttgtcaac agaggcaaag      1708
109     ttaagcttga tgatgggtta aatcggtttg atagcaccat gggacatttt tttaacaaaa      1768
110     ataaatgcat gaagagacat agccttttag ttttgctaag tgtgaaatgg aaatgcttta      1828
W--> 111     caggaagtaa atgcaaatta nttttaagtg tgcttttaaag aaaaatattt tccccacagg      1888
112     agaaatttaa ataaagaatt ttatttggtg aa                                1920
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115 <211> LENGTH: 362
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 2
119     Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
120     1              5              10              15
121     Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
122     20              25              30
123     Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
124     35              40              45
125     Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
126     50              55              60
127     Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
128     65              70              75              80
129     Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
130     85              90              95
131     Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
132     100             105             110
133     Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
134     115             120             125
135     Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
136     130             135             140
137     Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
138     145             150             155             160
139     Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu
140     165             170             175
141     Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys
142     180             185             190
143     Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu

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Input Set : N:\paola\US09697863A.RAW

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144          195          200          205
145      Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr
146          210          215          220
147      Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln
148      225          230          235          240
149      Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr
150          245          250          255
151      Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg
152          260          265          270
153      Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly
154          275          280          285
155      Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn
156          290          295          300
157      Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe
158      305          310          315          320
159      Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
160          325          330          335
161      Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp
162          340          345          350
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164          355          360
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167 <211> LENGTH: 1312
168 <212> TYPE: DNA
169 <213> ORGANISM: Mus musculus
170 <220> FEATURE:
171 <221> NAME/KEY: CDS
172 <222> LOCATION: (122)..(1234)
173 <223> OTHER INFORMATION:
174 <400> SEQUENCE: 3
175      agctattaat gattcgaatt tatacgactc actataggga atttggccct cgaggccaag      60
176      aattcggcac gagggcggga agcagcgtga agagcgggtg ttttgagggg accctgcggc      120
177      g atg gcg tct ggc agc agt tcc gat gcg gcg gag ccc gca ggg ccg gca      169
178      Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
179      1          5          10          15
180      ggg cgg gcg gcg tcg gcg ccc gaa gca gca cag gcg gag gag gac cgg      217
181      Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
182          20          25          30
183      gtg aag agg cgg cgg ctt cag tgc ctg ggc ttt gcg ttg gtg ggg gga      265
184      Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
185          35          40          45
186      tgc gac ccc acg atg gtc ccc agc gtc ctg cgg gag aac gac tgg cag      313
187      Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
188          50          55          60
189      acg cag aaa gcc ctg agc gcc tac ttc gag ctg cca gag aac gac caa      361
190      Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
191      65          70          75          80
192      ggg tgg ccg cgc cag cct ccc acg tcc ttc aag tcc gag gcc tat gtt      409
193      Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val

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194		85	90	95	
195	gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt				457
196	Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser				
197		100	105	110	
198	cca tct gga act cct cta gaa gat agc agc act att tct ttc att acc				505
199	Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr				
200		115	120	125	
201	tgg aat att gat gga tta gat gga tgc aat ctg ccc gag agg gct cga				553
202	Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg				
203		130	135	140	
204	ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta				601
205	Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu				
206		145	150	155	160
207	cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc				649
208	Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala				
209		165	170	175	
210	agt tac aca att att aca ggt aat gaa gaa gga tat ttc aca gct ata				697
211	Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile				
212		180	185	190	
213	cta ttg aag aaa gga aga gtg aaa ttt aaa agt cag gag att att cct				745
214	Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro				
215		195	200	205	
216	ttt cca aat acc aaa atg atg aga aac ctg cta tgc gta aat gtg agt				793
217	Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser				
218		210	215	220	
219	ttg ggt gga aat gaa ttt tgc ctt atg aca tcc cat ttg gag agc acc				841
220	Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr				
221		225	230	235	240
222	aga gaa cat tct gcg gaa cga ata aga caa tta aaa act gtt ctt gga				889
223	Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly				
224		245	250	255	
225	aaa atg caa gag gct cca gat tca acc acg gtt ata ttt gca gga gat				937
226	Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp				
227		260	265	270	
228	aca aat tta aga gat caa gaa gtt atc aaa tgt ggt ggt tta cct gac				985
229	Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp				
230		275	280	285	
231	aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag				1033
232	Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln				
233		290	295	300	
234	tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct				1081
235	Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala				
236		305	310	315	320
237	tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag ggg cac				1129
238	Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His				
239		325	330	335	
240	ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt				1177
241	Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys				
242		340	345	350	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/17/2002
PATENT APPLICATION: US/09/697,863 TIME: 14:13:59

Input Set : N:\paola\US09697863A.RAW
Output Set: N:\CRF4\09172002\I697863.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1627,1849
Seq#:5; N Pos. 1392,1530,1531
Seq#:5; Xaa Pos. 395,441
Seq#:6; Xaa Pos. 395,441

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:6; Line(s) 419

VERIFICATION SUMMARY

DATE: 09/17/2002

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TIME: 14:13:59

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L:4 M:270 C: Current Application Number differs, Wrong Format

L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1588

L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1828

L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1384

L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1432

L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1528

L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1536

L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:384

L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:432